

H	S	P	S	P	T	A	L	F	-C	L										
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC	ATG	TCT	CCA	TCC	CCG	ACC	GCC	CTC	TTC	TGT	CTT									
G	L	C	L	G	R	V	P	A	Q	S	G	P	L	P	K	P	S	L	Q	
GGG	CTG	TGT	CTG	GGG	CGT	GTG	CCA	GCG	CAG	AGT	GGG	CCG	CTC	CCC	AAG	CCC	TCC	CTC	CAG	
A	L	P	S	S	L	V	-P	L	E	-K	P	-V	T	L	R	C	Q	G	P	
GCT	CTG	CCC	AGC	TCC	CTG	CTG	CCC	CTG	GAG	AAG	CCA	GTG	ACC	CTC	CGG	TGC	CAG	GGA	CCT	
P	G	V	D	L	Y	R	L	E	K	L	S	S	S	R	Y	Q	D	Q	A	
CCG	GCC	GTG	GAC	CTG	TAC	CGC	CTG	GAG	AAG	CTG	AGT	TCC	AGC	AGG	TAC	CAG	GAT	CAG	GCA	
V	L	F	I	P	A	H	K	R	S	L	A	G	R	Y	R	C	S	Y	Q	
GTC	CTC	TTC	ATC	CCG	GCC	ATG	AAG	AGA	AGT	CTG	GCT	GGG	CGC	TAC	CGG	TGC	TCC	TAC	CAG	
N	G	S	L	H	S	L	P	S	D	Q	L	E	L	V	A	T	G	-V	.F	
AAC	GGA	AGC	CTC	TGG	TCC	CCC	AGC	GAC	CAG	CTG	GAG	CTC	GTT	GCC	ACG	GGA	GTT	TTT		
A	K	P	S	L	S	A	Q	P	G	P	A	V	S	S	G	G	D	V	T	
GCC	AAA	CCC	TCG	CTC	TCA	GCC	CAG	CCC	GGC	CCG	GGC	GTG	TCG	TCA	GGA	GGG	GAC	GTA	ACC	
L	O	C	Q	T	R	Y	G	F	D	Q	F	A	L	Y	K	E	G	D	P	
CTA	CAG	TGT	CAG	ACT	CGG	TAT	GGC	TTT	GAC	CAA	TTT	GCT	CTG	TAC	AAG	GAA	GGG	GAC	CCT	
A	P	Y	K	N	P	E	R	W	Y	R	A	S	F	P	I	I	T	V	T	
GCG	CCC	TAC	AAG	AAAT	CCC	GAG	AGA	TGG	TAC	CGG	GCT	AGT	TTC	CCC	ATC	ATC	ACG	GTG	ACC	
A	A	H	S	G	T	Y	R	C	Y	S	F	.S	S	R	D	P	Y	L	W	
GCC	GCC	CAC	AGC	GGA	ACC	TAC	CGA	TGC	TAC	AGC	TTC	TCC	AGC	AGG	GAC	CCA	TAC	CTG	TGG	
S	A	P	S	D	P	L	E	L	V	V	T	G	T	S	V	T	P	S	R	
TCG	GCC	CCC	AGC	GAC	CCC	CTG	GAG	CTT	GTG	GTC	ACA	GGA	ACC	TCT	GTG	ACC	CCC	AGC	CGG	
L	P	T	E	P	P	S	S	V	A	E	F	S	E	A	T	A	E	L	T	
TTA	CCA	ACA	GAA	CCA	CCT	TCC	TCG	GTA	GCA	GAA	TTC	TCA	GAA	GCC	ACC	GCT	GAA	CTG	ACC	
V	S	F	T	N	K	V	F	T	T	E	T	S	R	S	I	T	T	'S	P	
GTC	TCA	TTC	ACA	AAC	AAA	GTC	TTC	ACA	ACT	GAG	ACT	TCT	AGG	ACT	ATC	ACC	ACC	AGT	CCA	
K	E	S	D	S	P	A	G	P	A	R	Q	Y	Y	T	K	G	N	L	V	
AAG	GAG	TCA	GAC	TCT	CCA	GCT	GGT	CCT	GCC	CGC	CAG	TAC	TAC	ACC	AAG	GGC	AAC	CTG	GTC	
R	I	C	L	G	A	V	I	L	I	I	L	A	G	F	L	A	E	D	W	
CGG	ATA	TGC	CGG	GCT	GTG	ATC	CTA	ATA	ATC	CTG	GGG	GGG	TTT	CTG	GCA	GAG	GAC	TGG		
H	S	R	R	K	R	L	R	H	R	G	R	A	V	Q	R	P	L	P	P	
CAC	AGC	CGG	AGG	AAG	CGC	CTG	CGG	CAC	AGG	GGC	AGG	GCT	GTG	CAG	AGG	CGG	CTT	CGG	CCC	
L	P	P	L	P	Q	T	R	K	S	H	G	G	Q	D	G	G	R	Q	D	
CTG	CGG	CCC	CTC	CGG	CGG	AAA	TCA	CAC	GGG	GGT	CAG	GAT	GGA	GGC	CGA	CAG	GAT			
V	H	S	R	G	L	C	S	*												
GTT	CAC	AGC	CGC	GGG	TTA	TGT	TCA	TGA												

FIGURE 1a

7853-234

CGCGTGAACCCCAAGGCAAGGTGTATGCCAAGGGAGGGATCATGGCATGGGAGGGGACTCAAGA	CTGGCGTGTGTGGAC	1134
CGTGGAAACGAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCGATGCTGCCCTCTCTGGTGTTC	CACTCAGGGAGCCG	1213
TTCGGCCAGTGTCTGTCTGTCTGCTGCCCTCTCTGTCTGAGGGCACCCCTCCATTGGGATGGAAGGA	ATCTGTGGAGAC	1292
CCACATCCTCTCCCTGCACACTGTGGATGACATGGTACCCCTGGCTGGACCACATACTGGCCTCTTCT	CAACCTCTCT	1371
AAATATGGGCTCCAGACGGATCTCTAAGGTCCCAAGCTCTCAGGGTTGACTCTGTCCATCTCTGTG	CAAAATCTCT	1450
GTGCTTCCCTTGGCCCTCTGTCTCTGTTCTGGTTCCAGAAACTCTCTACCCCTCACTCCATCTCC	ACTGCGGTC	1529
TAAACAAATCTCTCTTGTCTCTCAGAACGGGTCTTGCAGGCAGTTGGGTATGTCAATTCAATTCTT	AGTGTGAAACT	1608
AGCACCGTTGCCCGCTTCCCTCACATTAGAAACAAAGATCAGCTGTGCAACATGGTCAAACCTCA	CTCTACCAACAA	1687
AAACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGCATCCCTATACTCCAGCAACTCGGGGGGCTG	AGGTGGGAGA	1766
ATGGCTTGACCTGGAGGCACAGGTTCCAGTGAGCTGAGATCACACCAACTGCACTCTAGCTGGG	TGACGAAGCCTGA	1845
CCTTGTCTCAAAATACAGGGATGAAATATGTCAATTACCCGTATTCATAGCACGTTGTATAACATG	TACTGCAAT	1924
TTGCTGTCCACCCATAAAATATGTACAATTATGTATAACATTAAATCATAAAAATAAGATAATGAA	AAAAAAAAAAAA	2003
AAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACAA		2047

FIGURE 1b

7853-234

(Sheet 3 of 42)

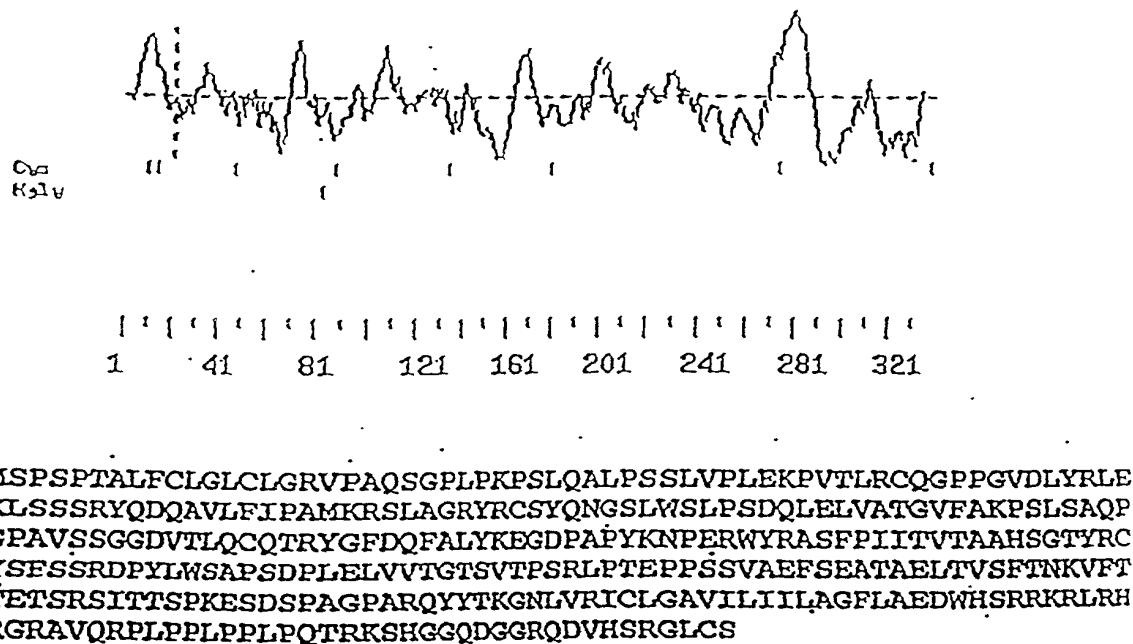


FIGURE 2

7853-234

ALIGN calculates a global alignment of two sequences
 version 2.0. Please cite: Myers and Miller, CABIOS (1989)
 > U91926 ORF 1893 aa vs.
 > ht268 ORF 1017 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 37.7% identity; Global alignment score: -8

10	20	30	40	50	60	70
inputs ATCACGCCGCCCTCACAGCCCTGCTCTGCCCTGGCTGAGTCTGGCCCCCAGGACCCCGTCAGGACAG						
ATGTCTCATCCCCGACGCCCTCTCTGCTTGGCTGCTCTGGCC-TGTGCCAGC-GCACAGTG						
10	20	30	40	50	60	
80	90	100	110	120	130	
inputs CGCCCTCCCCAACCCACCCCTCTGGCTGAGCCAGGCTCTGTAT-CAGCTGGGGAGCCCCGTGACCA						
CAACCGCTCCCCAACGCCCTCCAGGCTCTGCCAGCTCCCTGGTCCCCCTGGAGARGCCA-GTCAACCC						
70	80	90	100	110	120	130
140	150	160	170	180	190	200
inputs TCTGGTCTAGGGGAGCCTGGAGCCCCAGGAGTACCGACTGGATAAGAGGGAAGCCCAGGCCCCCTGG						
TCGGTGCAGGG--ACCT-----CCGGCGTG--GACCTGTA-----CCGCTGGAG---AAG						
140	150	160	170	180	190	200
210	220	230	240	250	260	270
inputs CAGAAATAACCCACTGGAACCCAGAACAGGCCAGATTCTCATCCATCCATGACAGAGCACCATGCG						
CTGACTT--CCAGCAGGTAC-AGGATCA-GGCAGTCCTCTCATCCGGCATGAAGAGAAGTCTGGCT						
190	200	210	220	230	240	
280	290	300	310	320	330	340
inputs GGGAGATAACCGCTGCCACTATTACAGCTCTGGAG--GCTGGTCAGAGGCCAGGCCCCCTGGAGCTGGT						
CGAACCTACCGCTGCTCTAC--CAGAACCGAAGCCTCTGGTCCCTGGCCAGGCCAGCTGGAGCTCGT						
250	260	270	280	290	300	310
350	360	370	380	390	400	410
inputs GATGACAGGATCTACAAACAAACCCACCTCTCAGCCCTGCGGAGGCCCTGTTGCTGAGGGGGAAAT						
TGCCACGGGAGTTTGCCAAACCCCTGGCTCTCAGCCCCAGCCCGGCCGGGGTCTGTCAGGGGGGAC						
320	330	340	350	360	370	380
420	430	440	450	460	470	480
inputs ATGACCCCTCCGATGTCACAGAACGGATATCACCATTTGTTCTGATGAAGGAGGGAGAACACAGC						
GTAACCTACAGTGTCTAGCTGGTATGCCATTGACCAATTGCTCTGTACAGGAGG						
390	400	410	420	430	440	
490	500	510	520	530	540	550
inputs TCCCGGGACCTGGACTCACAGCAGCTCACAGTGGGGTCCAGGGCGCTGTCCTGTCGGCCCOGT						
.....						

FIGURE 3a

7853-234

-----GGACCCCTG-----C-----GCCCTA-----CAA
 450 460
 560 570 580 590 600 610 620
 inputs GAACCCAGCCACACGGTGGAGGTTACATGCTATTA
 CCAACACCCCCCAGGTGCTGGTCCCAC
 :::: ::::: :::::: :: :::: :::::: :::::
 GAATCCCGA-----CAGATGGTAC-CGGGCTAGT-----TT-----CCCCAT-----CAT
 470 480 490 500
 630 640 650 660 670 680 690
 inputs CCCAGTGACCCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCCTCAGGGC
 :: :::::: :: :::::: :::
 CACGGTGACCGCC-----GCCACAG
 510 520
 700 710 720 730 740 750 760
 inputs CTGTCCTGGCCCCCTGGGCAGAGCCTGACCCCTCCAGTGTGGCTCTCATGTCGGCTACGACAGATTGTTCT
 :::::: :::::: :::::: :::::: :::::
 CGGAACCTA-----CCGATG-----CTACAGC-----TTCT
 530 540 550
 770 780 790 800 810 820 830
 inputs GTATAAGGAGGGGGAACTGACTTCCCTCCAGGGCCCTGGCCAGGCCCCAGGCTGGCTCTCCAGGGC
 :::::::
 CCAGCAG-----
 840 850 860 870 880 890 900
 inputs AACTTCACCCCTGGCCCCCTGTGAGCCCCCTCCCAGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
 :::::::
 GGACCCA-----TACCT--
 560
 910 920 930 940 950 960 970
 inputs CCTCCGACTGGCTGGCCCCCAGCGACCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGCTC
 :::::: :::::: :::::: :::::
 CTGGTOGGCCCCCAGCGACCCCTGGA-----GCT-----TGTG-----
 570 580 590 600
 980 990 1000 1010 1020 1030 1040
 inputs CCTGTCAGCACGCCGGGGGGGGACAGTGGCCTCAGGAGAGACCGTGAACCTGCTGTCAGTCATGGTGG
 :::: :::: :::: :::::
 CTCA-----CAGGAACCTCTGTGACCC-----CCCAGC-----CGGT-----
 610 620 630
 1050 1060 1070 1080 1090 1100 1110
 inputs CACTTTCACCTTCTCTGACCAARGAAGGGGAGCCCATCCCCCAGTGGCTCTGAGATCAATGTA
 :::::: :::::
 TACCAACAGAAC-----CA-----OCTTCC-----TOG-----
 640 650
 1120 1130 1140 1150 1160 1170 1180

FIGURE 3b

7853-234

Inputs GAGCTCATAGTACCAAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCCACGGGGGGACCTACAGGTG
 :... :...:
 GTA-----GCAGAATTCTC-----AGAAGGCAC-----CGCTGA-----ACTG--A
 660 670 680 690

1190 1200 1210 1220 1230 1240 1250
 Inputs CTACGGCTCATACAGCTCCACCCCCACCTGCTGCTTTCCCCAGTGAGCCCCCTGGAACTCATGGTCTCA
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 C---CGTCTCATTCACAAAC-----AAAGTCTT---CACAA-----CTGAGACT-----TCT--
 700 710 720 730

1260 1270 1280 1290 1300 1310 1320
 Inputs GGACACCTCTGGAGGCTCCACGCCACGGGCGCCCTCCACACCTGGTCTGGAGAGATAACCTGG
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 -----ACGACTATC---ACCACCACTCCACAGGA---GTCAGACTCTCCAG---CTGG-----
 740 750 760 770

1330 1340 1350 1360 1370 1380 1390
 Inputs AGCTTTCTGCGCTCTCGGTGGCTTCGCTGCTCTCCCTCCCTCCCTCCCTCCGACG
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 -----TCCTGC-----CCGCCAGTA---CTACACCAAGG
 780 790 800

1400 1410 1420 1430 1440 1450 1460
 Inputs TCAGCCCTCACAGCAACACAGGACATCTGACCAAGAGAAAGACTGATTTCCAGGGTCTCCAGGGGCTGCG
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 GCAAC-----CTGGTC-----CGGATAT---GCCTC-----GGGGCTG--
 810 820 830

1470 1480 1490 1500 1510 1520 1530
 Inputs GAGACACAGCCCAAGGACAGGGGCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCACGAGAAAACC
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 -----TGATCCTAATAA---TCCTG---CCGGGGTTCTG-----GCAGA-GGACTGG-----C
 840 850 860 870

1540 1550 1560 1570 1580 1590 1600
 Inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG---ACAGGGTGGAGCTGGACAGT---CAGACCCACACGAT
 :...:...:...:...:...:...:...:...:...:...:...:...:...:...:
 AC-----ACCGG---GAGGAAGGCGC---CTGGGGCAGGG---GCAGGGCTGTCAGAGGCGCT---
 880 890 900 910 920

1610 1620 1630 1640 1650 1660 1670
 Inputs CAAGACCCCCAGGCAGTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGCCCTCTCC
 :...:...:...:...:...:...:...:
 -----TCC-----CCCCCTG-----CGC-----C
 930 940

1680 1690 1700 1710 1720 1730 1740
 Inputs CCTCCCTCACTGTCGGGAAATCCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACAC
 :...:...:...:...:...:...:...:
 CCTCCO-CCGAGAC-----CGCGAAATCA---CA---GGG-----GTCAGG---ATGGA---
 950 960 970 980

FIGURE 3c

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1750 1760 1770 1780 1790 1800 1810
inputs TGAGGCTGCTCATCTGAAGCCTCCAGGAATGACCTACGCCAGCTGCACAGCTTGACCCCTAGACGG
:::
---GGC-----CGAC-----ACGATCTT-----CAGC-----CG-
990 1000

1820 1830 1840 1850 1860 1870 1880
inputs AAGGCAACTGAGCCTCCATCCCAGGAAGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
:::
-----CGGGTTATG-----TTCA-----
1010

1890
inputs CCATCCAC

FIGURE 3d

ALIGN calculates a global alignment of two sequences
 version 2.0u Please cite: Myers and Miller, CABIOS (1989)

> hT268 a.a. 339 aa vs.
 > GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
 scoring matrix: pam120.mat, gap penalties: -12/-4
 23.0% identity; Global alignment score: -642

10	20	30	40	50	60	
inputs MSPSPITALFCLGLCLG-RVPAQSGPLPRPSLQALPSSLVPLERPVTLRCQGPPGVLDYRLEKLSSS-----						
10	20	30	40	50	60	
inputs MTPALTALLCLGLSLCPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIHCOGSLEAQEYRLDKEGSPEPLD						
10	20	30	40	50	60	
70	80	90	100	110	120	130
inputs RYQ-----DQAVLFIPAKRSLAGRYRCSYQNGSLHSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV						
80	90	100	110	120	130	140
inputs RNIKPLEPKXKARFSIPTSHENHACRYRCHYSSAGHSEPSDPLELVMFTGFYNKPTLSALPSPVVASGGNH						
150	160	170	180	190	200	210
inputs TLQCQT-----RY-----						
140	150					
inputs -----CFDQFALYKEGDP-----						
220	230	240	250	260	270	280
inputs SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDORFVLYKEGERDFLQRPGQQPQAGLSQAN						
290	300	310	320	330	340	350
inputs -----APYK-----NP-----ERW-----						
360	370	380	390	400	410	420
inputs -----YRASFPPIITVTAHSGTYRCYSFSSRDPYLHSAPSQDPLELVTG						
380	390	400	410	420		
inputs FOTFLLTKEGAHKPPLRLRSHYGAHKYQAEFPHSPTSAHAGTYRCYGSYSSNPHLLSFSEPLELHVSG						
430	440	450	460	470	480	490
inputs -----210 220 230 240 250 260-----						
inputs TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF-----TTETRSITTPKESD--SPAGPA-						
430	440	450	460	470	480	490
inputs HSGGSSLPPPTGPPSTPGLGRYLEVLIGVSVAFLLLFLLRRQRHSKHTSDQRKTDQFQRPAAGAE						
430	440	450	460	470	480	490
inputs RQYTTKGHLVRICLGAVIL-----IILAGFLAEDW-----HSRRKR-----						
430	440	450	460	470	480	490

FIGURE 4a

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TEPKDRGLRRSSPAADVQEENLYAAVKDTQS	EDRVELDSQSPH	HDEDPQAVTYAPVKHSSPRREM	ASPPS					
500	510	520	530	540	550	560		

300	310			320	330			
inputs	-----	LRHRGRAVQ	--RPL-----	PPLPPLPQTRK	-----	SHGGQDGGRQDVHSRGLC		
:		
SLSGEFLOTKDRQVEEDRQMDTEAA	SEASQDV	TYAQLHS	LT	RRKATE	PPPSQE	GEP	PAEPSIY	ATLAI
570	580	590	600	610	620	630		

inputs	S							

FIGURE 4b

Alignments of top-scoring domains:
ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1

ht268 41 *->GesvtLtcsvsgfgppgvsvtWvfkgk.lgpsllgyssysrlesgk
 + v tL+C+ + v y + k + + r++ +
 EKPVTLRCQGP-----PGVDLY-RLEK1SS-----RYQDQ-- 70

ht268 71 anlsegtrfsissltLtissvekeDsGtYtCvv<-+
 +tL i +++ +G Y+C
 -----AVLFIPAMKRSLAGRYRCSY 90

FIGURE 5A

sig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
*->GesvtLtcsvsgfgppgvsvtkyfkngk.lgpsllgysysrlesgek
G++vtL+C++ + ++ y k+g++ + y++
ht268 127 GGDVTLQCQTR---YGFDFQFALY-KEGDpAP-----YKNPERWYR-- 162
anlsegrfsissltLtissvekeDsGtYtCvv<-
+++i++v++ sGtY+C
hT268 163 -----ASFPIITVTAHHSGTYRCYS 182

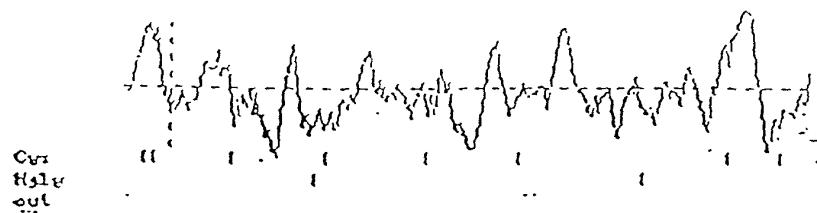
FIGURE 5B

	H	S	P	A	
GAGTCGACCCACGGCGTCGGCTCCCTGCTGGCCACATGGCTGGACTGGGTGGCAGAAC	ATG	TCT	CCA	GGC	4
TCA CCC ACT. TTC TTC TGT ATT CGG CTG TGT GTC CTC CAA GTG ATC CAA ACG AGT GGC					74
P L P K P S L Q F Q P S S L V P L G Q S					24
CCA CTC CCC AAC CCT TCC CTC CAG CCT CAG CCC AGT TCC CTG GTC CCA CCC CTC CCT CAG TCA					134
V I L R C Q G P P D V D L Y R L E K L K					44
GTT ATT CTG AGG TGC CAG GGA CCT CCA CAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA					194
P E K Y E D O D F I P T H E R S N A					64
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT					254
G R Y R C S Y Q H G S H W S L P S D Q L					104
CGA CGG TAT CGA TGC TCT TAT CAG AAT CGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT					374
E L I A T G V Y A K P S L S A H P S S A					124
GAG CTA ATT GCT ACA CGT GTG TAT CCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA					434
V P Q G R D V T L K C Q S P Y S F D E F					144
GTC CCT CAA CGC AGG GAT GTG ACT CTG AGG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC					494
V L Y K E G D T G P Y K R P E K H Y R A					164
GTT CTA TAC AAA GAA CGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC					554
N F P I I T V T A A H S G T Y R C Y S F					184
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT CGG ACG TAC CGG TGT TAC AGC TTC					614
S S S S P Y L W S A P S D P L V L V V T					204
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CGG ACT GAC CCT CTA GTG CTT GTG GTT ACT					674
G L S A T P S Q V P T E E S F P V T E S					224
CGA CTC TCT GCC ACT CCC AGC CAG GTC CCC AGC GAA TCA TTT CCT GTG ACA GAA TCC					734
S R R P S I L P T N K I S T T E K P H N					244
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT					794
I T A S P E G L S P P I G F A H Q H X A					264
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC					854
K G N L V R I C L G A T I I I I L L G L					284
AAG GGG AAT CTG GTG CGG ATA TGC CTT GGT GCC AGC ATT ATA ATA ATT TTG TTG GGG CTT					914
L A E D H H S R K K C L Q H R H R A L Q					304
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA					974
R P L P P' L P L A					314
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG					1004
AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGGACATCACCACTAGAGCCACAGACAT					1083
GGACATACAGAGTGGGGAGGTATATATATGAGTGTGGAGAATAATGCAAGGCCAACAGGTGAAAAAAA					1162
A					1163

FIGURE 6

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1 41 81 121 161 201 241 281

MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQONGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTTEESFPVTESSRRPSILPTNKISTTE
KPMNTASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

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(Sheet 14 of 42)

ALIGN calculates a global alignment of two sequences
 version 2.0. Please cite: Myers and Miller, CABIOS (1989)

> U91928 ORF 1893 aa vs.
 > mT268 ORF 939 aa

scoring matrix: pam120.mat, gap penalties: -12/-4
 34.3% identity; Global alignment score: -836

10 20 30 40 50 60 70
 inputs ATGACCCCCCCCCCTCACAGCCCCCTCTGGCCCTGGGCTGAGCTGCTGGCCCCAGACACCCCCCTGCAAGGCAC
 ::::: :: :::: ::::: :: :::: ::::: :::::
 ATGTCTCCAGCC-TCAC-CC---ACTTTCTT---CTGTAT-----
 10 20 30

80 90 100 110 120 130 140
 inputs CGCCCTTCCCCAAACCCACCCCTGGGCTGAGCCAGGGCTGTGATCAGCTGGGGAGCCCCGTGACCAT
 ::::::: ::::::: :::::::
 -----TGGGCTG-----TGTGTACTGC-----
 40

150 160 170 180 190 200 210
 inputs CTGGTGTCAAGGGAGCCCTGGAGGGCCACGGACTACCGACTGGATAAAGAGGGAGCCCCACAGCCCCCTGGAC
 ::::::: ::::::: :::::::
 -----AAGTGATCC-----AAACACACAC-----TGG-----
 50 60 70

220 230 240 250 260 270 280
 inputs AGAAATAACCCACTGGAACCCAGAACAGGGCCAGATTCTCCATCCCATCCATGACAGACCCATGGCG
 ::::: ::::: ::::: ::::: ::::: :::::
 -----CCCACT---CCC---CAAG-----CCTTCCC-TCCAGG-----
 80 90

290 300 310 320 330 340 350
 inputs GGAGATAACCCCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCCAGCGACCCCTGGAGCTGGTGTAT
 ::::::: ::::::: ::::::: ::::::: :::::::
 -----CTCAGCC-----CAGTCCCTG-CTACCCCTGGGTCAAG-----
 100 110 120

360 370 380 390 400 410 420
 inputs GACAGGATTCTACAACAAACCCACCCCTCTCAGCCCCCTGGCCAGGGCTGGCTCAGGGGGAAATATG
 ::::: ::::: :::::
 -----TCAG---TTATTC-----TGAGGTG-C-CACCGA-----
 130 140 150

430 440 450 460 470 480
 inputs ACCCTCC-GATGTGGCTCACAGAACGGATATCACATTCTGGCTGAGGAACGAGACACCCAGCTC
 ::::::: ::::::: ::::::: ::::::: :::::::
 -----CCTCCAGATGTGG-----ATTATATACGCTGGAGAACCTGAAA-----
 160 170 180 190

490 500 510 520 530 540 550
 inputs CCGGGAGACCTGGACTCACAGCAGCTCCACAGCTGGGGGGTCCRGCCCTGTTCCCTGCGGGCCCCGTGA
 ::::::: :::::
 -----CCGGGAGACCTGGACTCACAGCAGCTCCACAGCTGGGGGGTCCRGCCCTGTTCCCTGCGGGCCCCGTGA-----

FIGURE 8a

FIGURE 8b

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Inputs GCTCATAGTACCAAGGCTGAATTCCCCATGACTCTGTGACCTCAGCCCACGGGGGACCTACAGGTGCT
 : : .
 G--AAATGGTACCGGCCAATTCCCCATCATCACAGTGACTCTGCTCACACTGGGACGTACCGTGT
 460 490 500 510 520 530 540

1190 1200 1210 1220 1230 1240 1250
 Inputs ACGGCTCATACAGCTCCAAACCCCCACCTCTCTTCCCCAGTGAGCCCCCTGGAACCTCATGGCTCTCAGG
 : .
 ACAGCTCTCCAGCTCATCTCATACCTGTGGTCAGCCCCGAGTGACCCCTCTAGTGCCTGGTTACTGG
 550 560 570 580 590 600 610

1260 1270 1280 1290 1300 1310 1320
 Inputs ACACCTGGAGGCTCCAGCTCCACACAGGGCCGCCCTCACACCCCTGGCTGGGACATACCTGGAG
 : .
 ACTCTCTG----CCA--CTCCCAGCC--AGGT--ACCCAC----GGA-AGAATCATTCTG----
 620 630 640 650 660

1330 1340 1350 1360 1370 1380 1390
 Inputs GTTTCAATTGGGTCTGGTGGCCTTCGCTGCTCTCTCTCTCTCTCTCTCTCCGACGTC
 : .
 ---TGA----CAGAATCCT---CCAGGAGACCTTCATC---TCTTAC---CCACAAACAA
 670 680 690 700

1400 1410 1420 1430 1440 1450 1460
 Inputs AGCGTCACAGCAAAACACAGGACATCTGACCAGAGAAGACTGATTCAGCGTCTGCAGGGGCTGCGA
 : .
 A---TATCTACAA---CTGAA---AAGCCTATGAATATC---ACTGCCT-C-TCCAG-AGGGGCTG----
 710 720 730 740 750

1470 1480 1490 1500 1510 1520 1530
 Inputs CACAGAGCCCAGGACAGGGGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCAGGAAGAAAACCTC
 : .
 ---AGCCCT----CC---AATTGGTTTGCTCATCAGCA----C
 760 770 780

1540 1550 1560 1570 1580 1590 1600
 Inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGCTGGAGCTGGACAGTCAGAGCCCACACGATGAG
 : .
 TATGC----CAAGGGAAATCTGGTC----CGGATATG
 790 800 810

1610 1620 1630 1640 1650 1660 1670
 Inputs ACCCCCCAGGCACTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCCTC
 : .
 ---CCTTGG----TCCCACAT----TATAATAATTGT----
 820 830 840

1680 1690 1700 1710 1720 1730 1740
 Inputs CTCACTGCTGGGAATTCTGGACACAGGACAGACAGGTGGAGAGGGACAGGAGATGGACACTGAG
 : .
 ---TGGGGCTT--CTAG--CAGAGGATTGGC----ACACTGGGAGAA----AT
 850 860 870 880

FIGURE 8c

```

1750      1760      1770      1780      1790      1800      1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCAGCTGCACAGCTTAGACGGAAAGG
      :: :::::..      :::::::..      ::::: ..      :::::
      GC--CTGCAACA-----CAGGATGAGA-----GCTTTGC-----AAAGG
      890          900          910

1820      1830      1840      1850      1860      1870      1880
inputs CAACTGAGCCTCTCCATCCCAGGAAGGGGAAACCTCCAGCTGAGGCCAGCATCTACGCCACTCTGGCCAT
      : :::.      :::::      :::::      :::::::
      CCACTA-----CCACC-----CCTCC-----CACTGGCC---
      920          930

1890
inputs CCAC

```

FIGURE 8d

ALIGN calculates a global alignment of two sequences
 version 2.0. Please cite: Myers and Miller, CABIOS (1989)

> mT268 a.a. 313 aa vs.
 > GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
 scoring matrix: pam120.mat, gap penalties: -12/-4
 20.31 identity; Global alignment score: -802

10 20 30 40 .50 60
 inputs HSPAPSPTFFCIGLCVLIQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVLDLYRLEKL-KPERRY
 :::: .
 MTPALTALLCGLSLGPGTRVQAGPFPKPTLWAEPGSVISHGSPVTIHCQGSLEAQEYRLDKEGSPEPLD
 10 20 30 40 50 60 70

 70 80 90 100 110 . . . 120 130
 inputs DQDFL-----F-IPTRERSKAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDV
 .. : : : .
 RNNPLEPKNPKARFSIPSMTHIAGRYRCHYSSAGHSEPSOPLELVHTGFYNYKPTLSALPSPVVASCGIM
 80 90 100 110 120 130 140

 inputs TLKC--QSPY-----
 ::: : :
 TLRCGSQKGYHVFVLMKEGEHQLPRTLDSQLHSGCFQALFPVGPVNPSPHRWRFICYYYYYHQTTPQVWSHP
 150 160 170 180 190 200 210

 140 150
 inputs -----SFDEFVLYKEGD-----
 .
 SDOPLEILPSGCSRKPSSLTLQGPVLAPGQSLTLQCGSDVGYDRFLYKEGERDFLQRPGQQPQAGLSQAN
 220 230 240 250 260 270 280

 160
 inputs -----TGPYK-----RP-----EKH-----
 .
 FTLGPVSPSHGCQYRCYCAHNLSSSEWSAPSOPLNILHAGQIYDTVSLSAQPGPTVASGENVILLCQSHHQ
 290 300 310 320 330 340 350

 170 180 190 200
 inputs -----YRANFPIITVTAAHSGTYRCYSFSSSSPYLKHSAPSOPLVLVVTG
 .
 FDTFLLLTKEGAAHPPPLRLRSHYCAHKYQAEFPHPSPVTSAAHAGTYRCYGSYSSNPKHLLSFPSEPLEKIVSG
 360 370 380 390 400 410 420

 210 220
 inputs LSATPSQVPTTEES-----FPV-----
 .
 HSGGSSLPPTPGPPSTPGLCRYLEVLIGVSVAFVLLLFLLLFLLRRQRHSKHTSDQRKTDQFQRPAGAAE
 430 440 450 460 470 480 490

 230 240 250 260 270
 inputs TESS-----RRPS-----ILPTNKISITEKPHNI-TASPEGLSP-PIGFAH-QHYAKGKILVR-I

FIGURE 9a

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FIGURE 9b

Alignments of top-scoring domains:
fig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4

*->GesvtLtcsvsgfgppgvsvtWYfkngk.lgpsllgysysrlesgek
mT268 42 G+sv L+C+ ++v y + k ++ +++e +
GQSVILRCQGP-----PDVDLY-RLERLKP-----EKYEDQ-- 71

anlsegrfsissltltissvekeDsGtYtCvv<-*
L i + e++++G Y+C
mT268 72 -----DFLFIPPTMERSNAGRYRCSY 91

FIGURE 10A.

ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
•->GesvtLtCsvsgfgppgvsvtWYfknigk.lgpsllgysysrlesgek
□T268 128 G +vtL C++ ++ Y k+g++ + y+r+e +
GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-----YKRPEKW-Y 162

anlseggrfsissltLtissvekeDsGtYtCvv<-
mT268 163 RA-----NFPIITVTAHSGTYRCYS 183

FIGURE 10B

ALIGN calculates a global alignment of two sequences
version 2.0u Please cite: Myers and Miller, CABIOS (1989)

> hT268 a.a. 339 aa vs.
> mT268 a.a. 313 aa

scoring matrix: psm120.mat, gap penalties: -12/-4K
64.4% identity; Global alignment score: 1011

10	20	30	40	50	60	
inputs	HSPSPPTALFCIGLCLGRV-PHQSGPLPKPSLQALPSSLVPLKEPKVTLRCQGPPGVLDYRLEKLSSSRYQD	
	HSPASPTFFCIGLCLQVQIQTQSGPLPKPSLQAQPSLVLQGQSVILRCQGPPDVLDYRLEKLKPEKYED	
10	20	30	40	50	60	
70	80	90	100	110	120	130
inputs	QAVLFIPAYKRSLAGRYRCSYQNGSLHWSLPSDQLELVTGFAKPSLSAQCPGPAVSSCGDVTLQCQTRYG
	QDFLFIPMTERSHAGRYRCSYQNGSLHWSLPSDQLELIAATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
80	90	100	110	120	130	140
140	150	160	170	180	190	200
inputs	FDQFALYKEGDPAPYKPNPERWYRASFPPIITVTAHSGTYRCYSFSSRDPYIWSAPSAPSDPLELVVTGTSVTP
	FDEFVLYKEGDTGPYKRPEKWWYRASFPPIITVTAHSGTYRCYSFSSSSPYIWSAPSAPSDPLVLTGSLATP
150	160	170	180	190	200	210
210	220	230	240	250	260	270
inputs	SLPLPTEPSSVAEFSEATAELTVSFTNKVTTETRSITTSKESDSPAGPARQYYTKGNLVRICLGAIV
	SQVPTEESFPVTESSRRPSILP---TNKISTTEKPHNITASPEGLSPPIGFAHQHYAKGNLVRICLGAIV
220	230	240	250	260	270	280
280	290	300	310	320	330	280
inputs	LILLAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
	IIILLLGLIAEDWHSRKRLQHRLQRLQPLPPLP-LA-----
290	300	310	320	330	280	290

FIGURE 11

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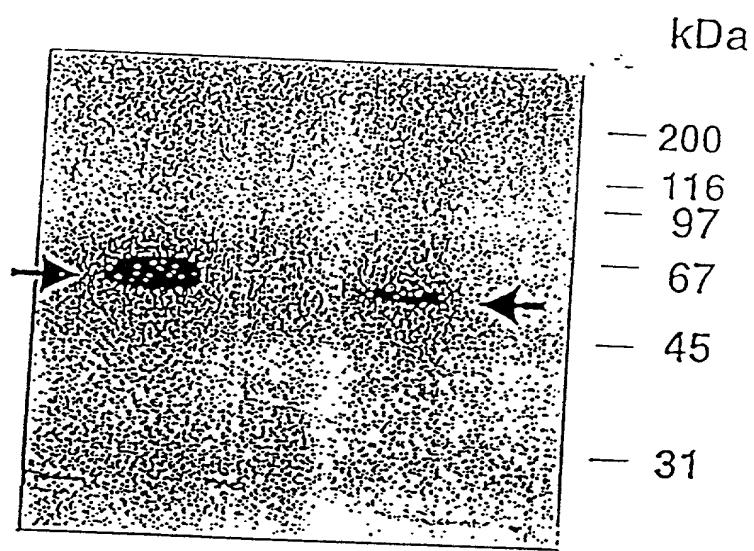


FIGURE 12

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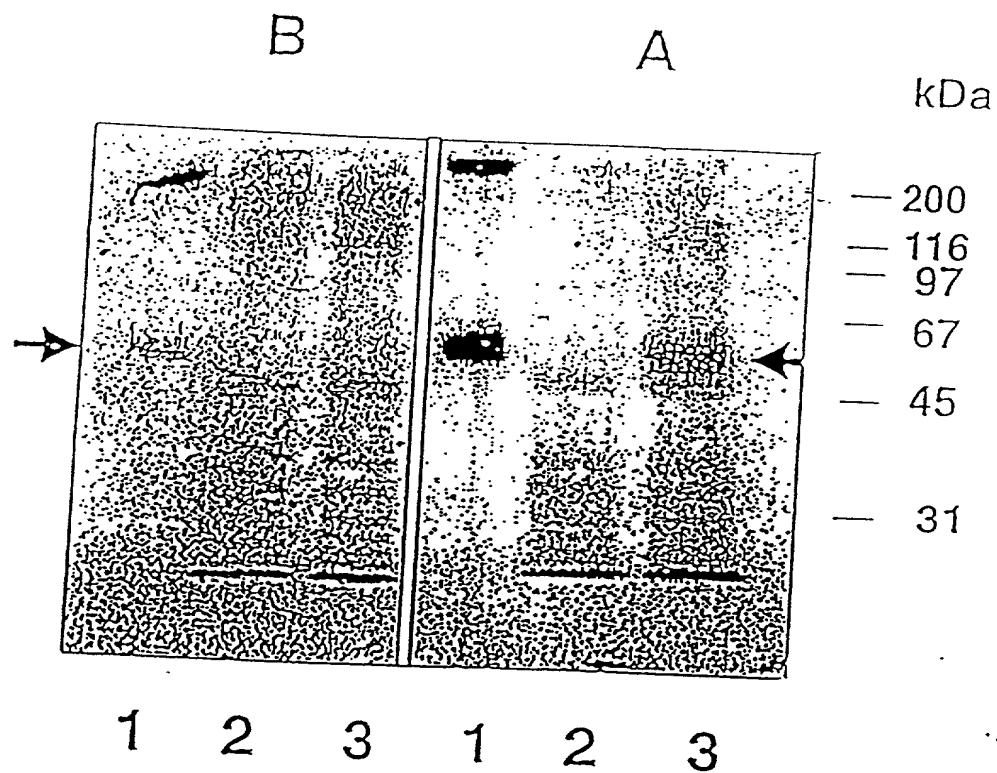


FIGURE 13

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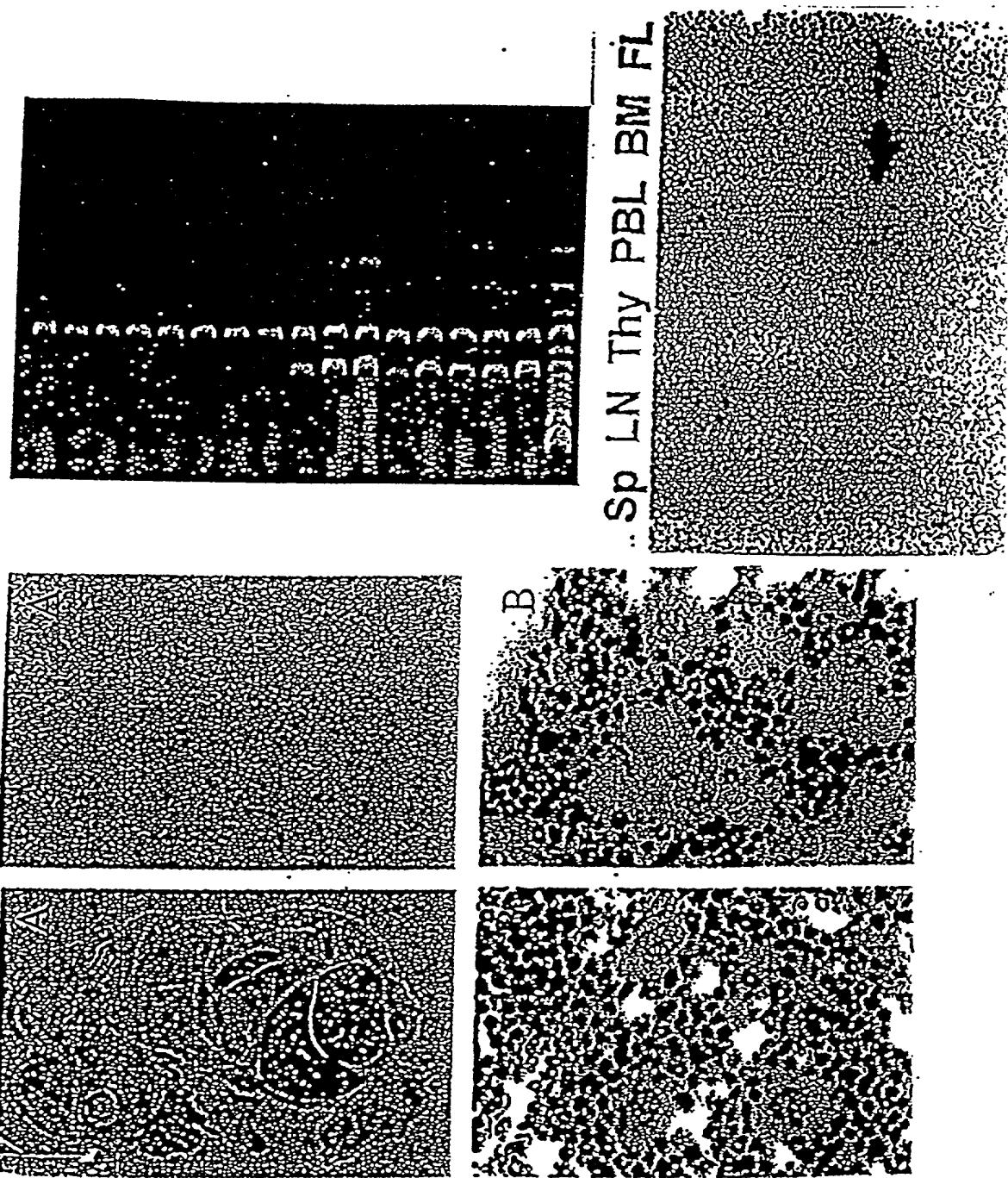


FIGURE 14

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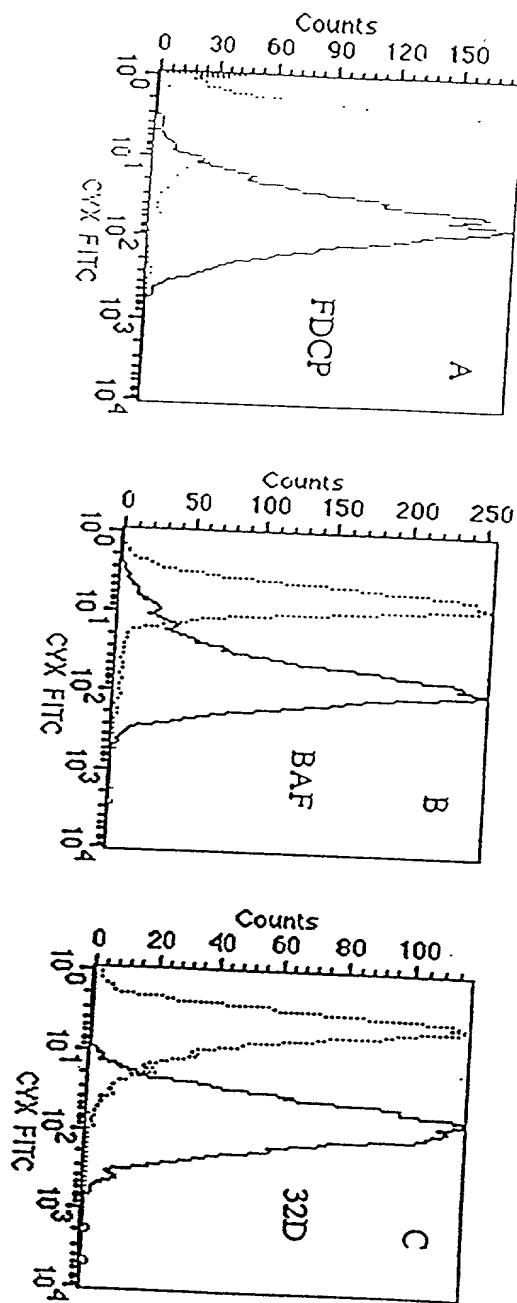


FIGURE 15

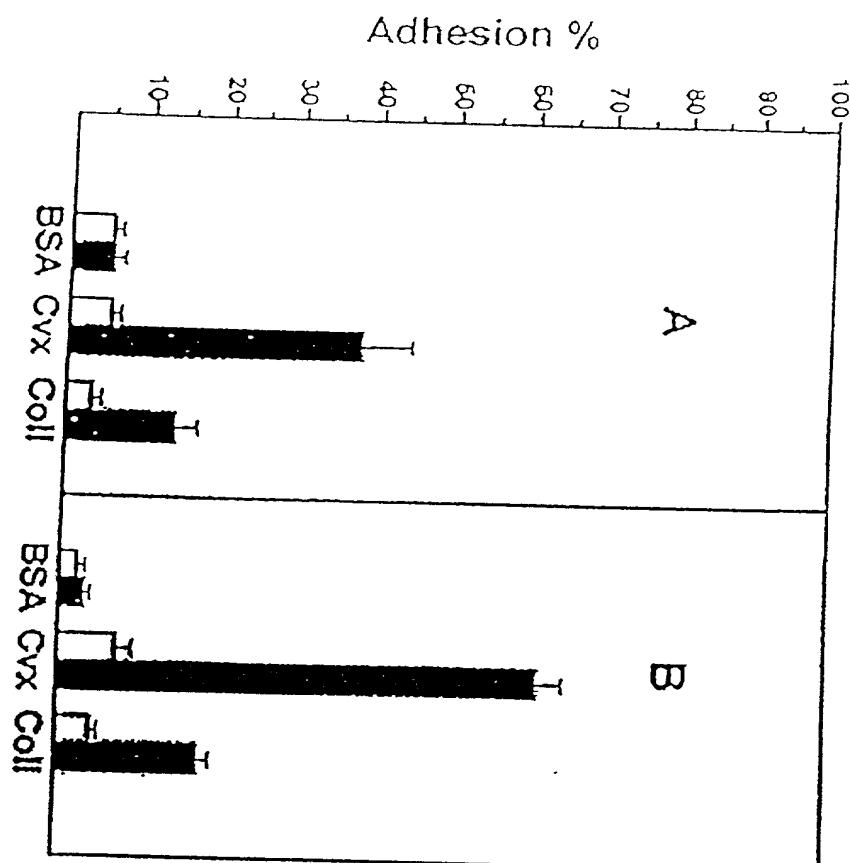


FIGURE 16

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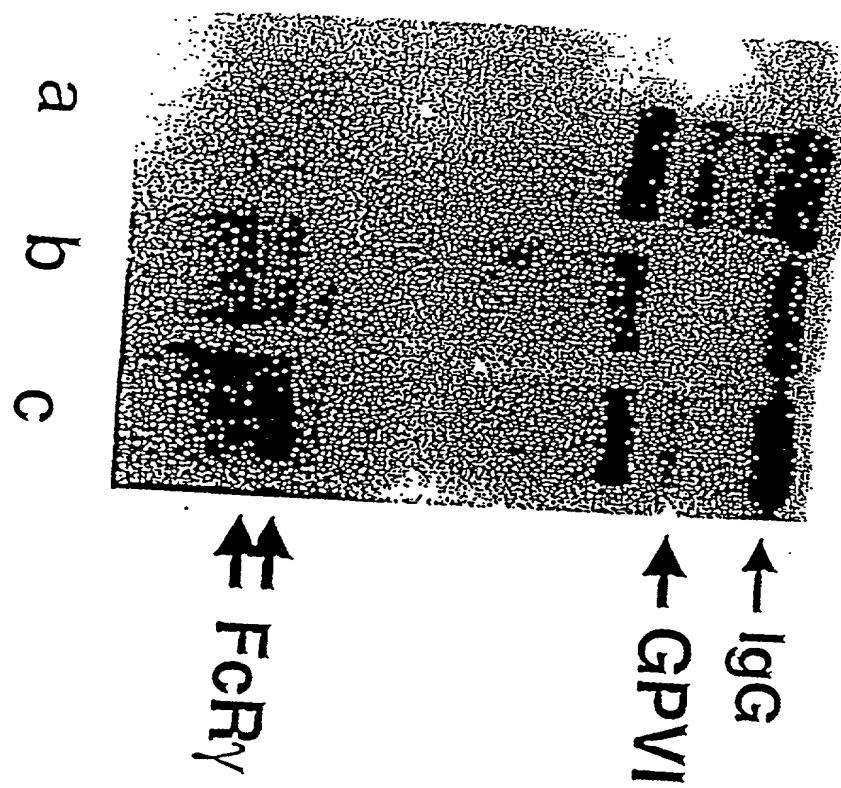


FIGURE 17

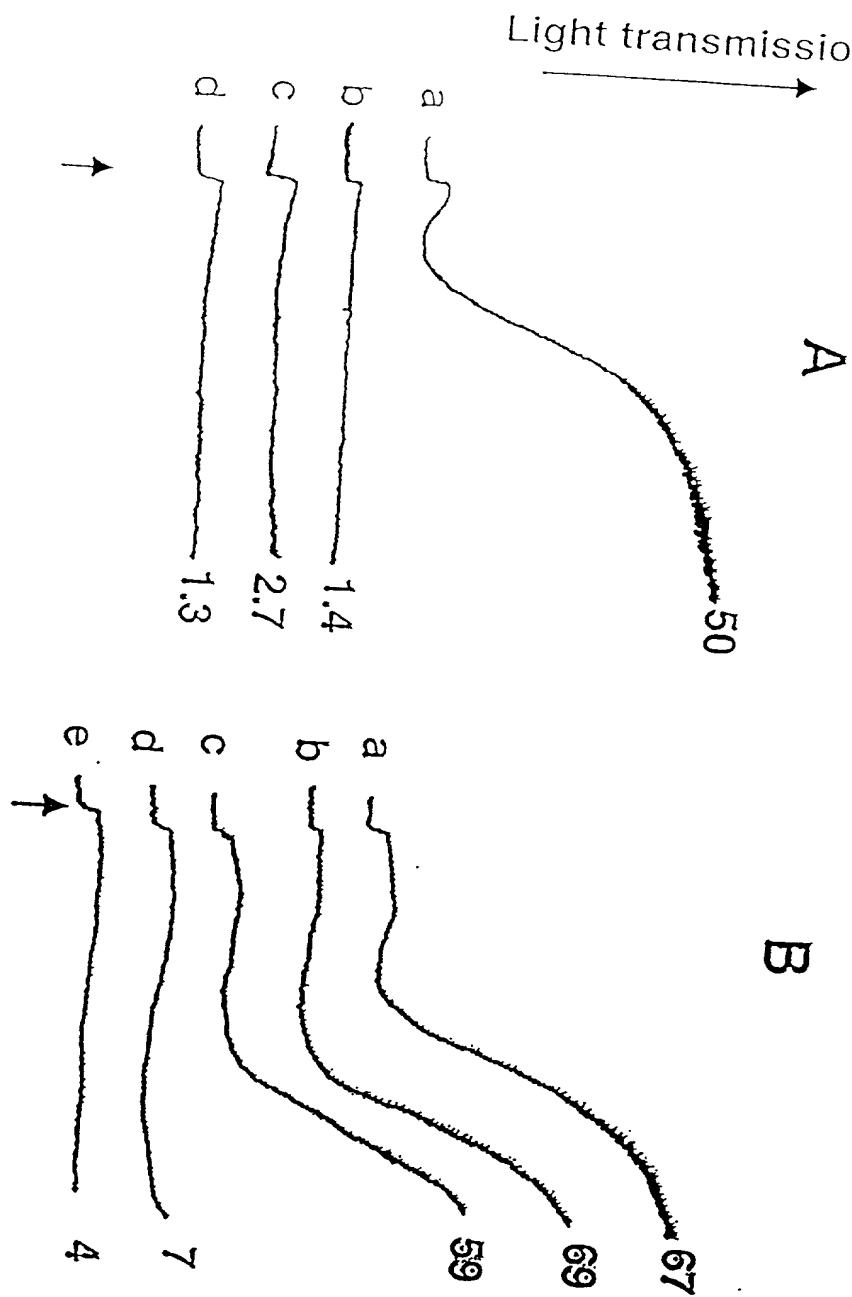


FIGURE 18

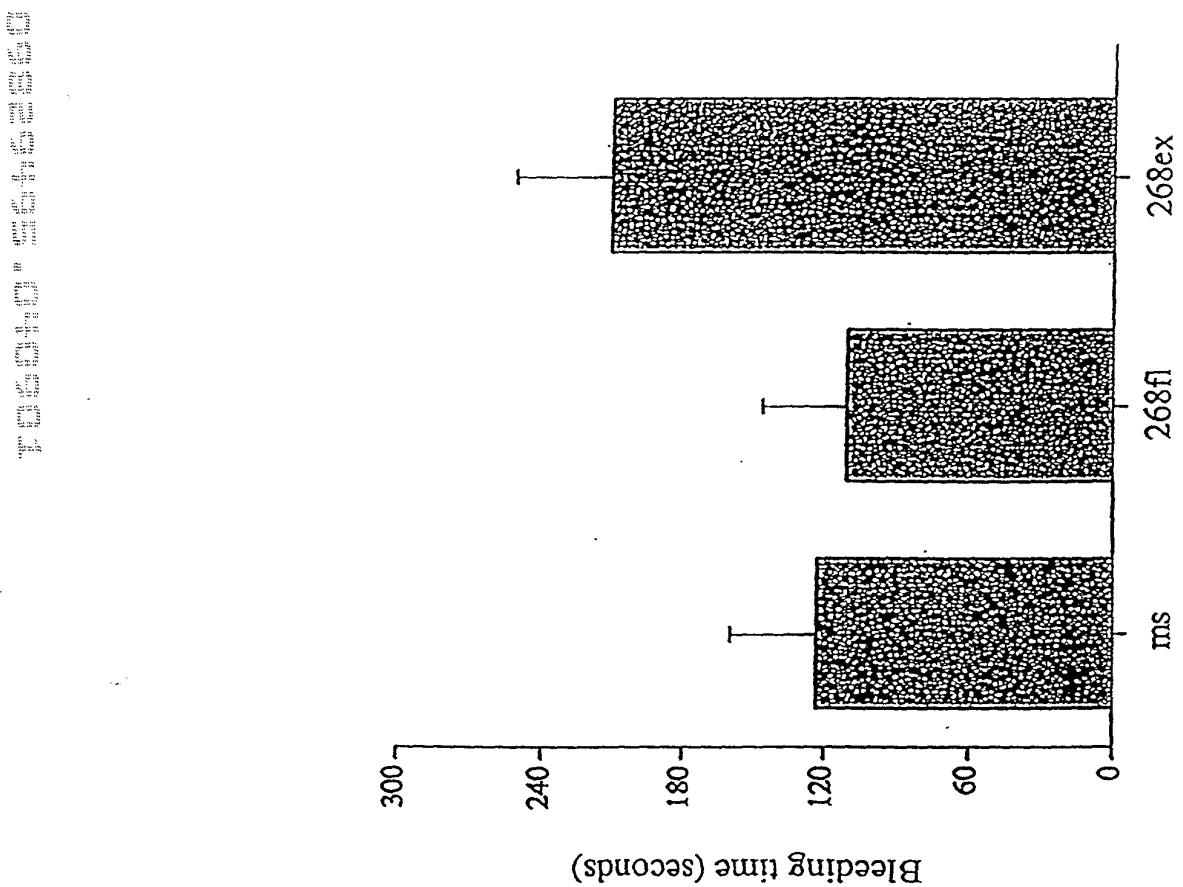
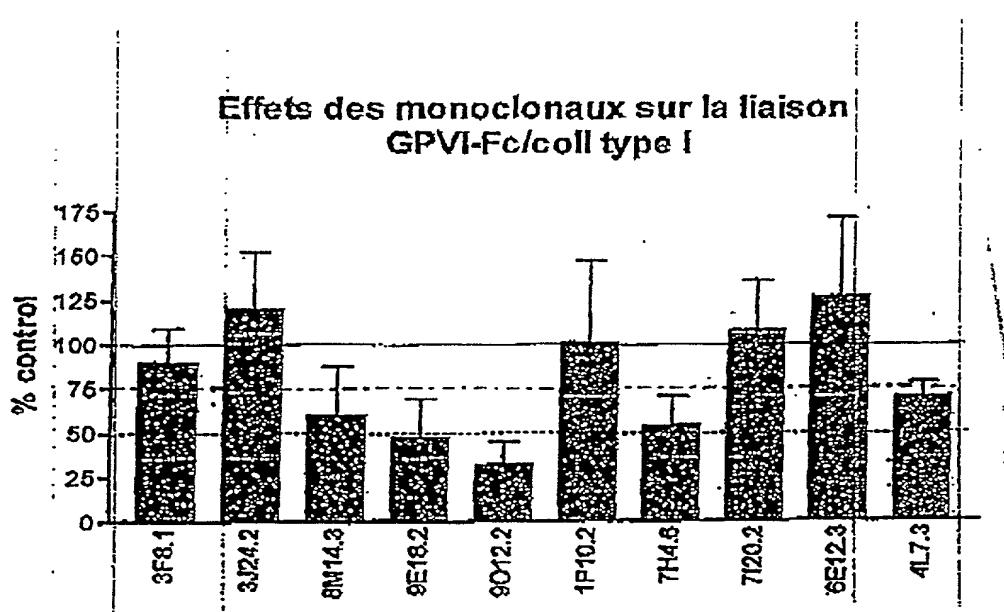


FIGURE 19

**FIGURE 20**

Effet des monoclonaux sur la liaison
GPII-Fc / Convulxine

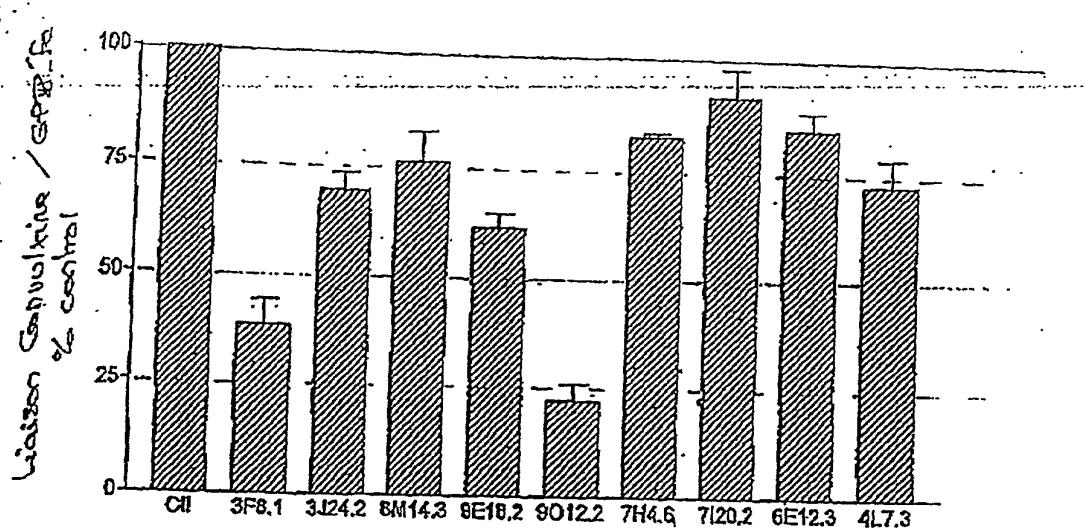


FIGURE 21

PBS collagen

Fab collagen

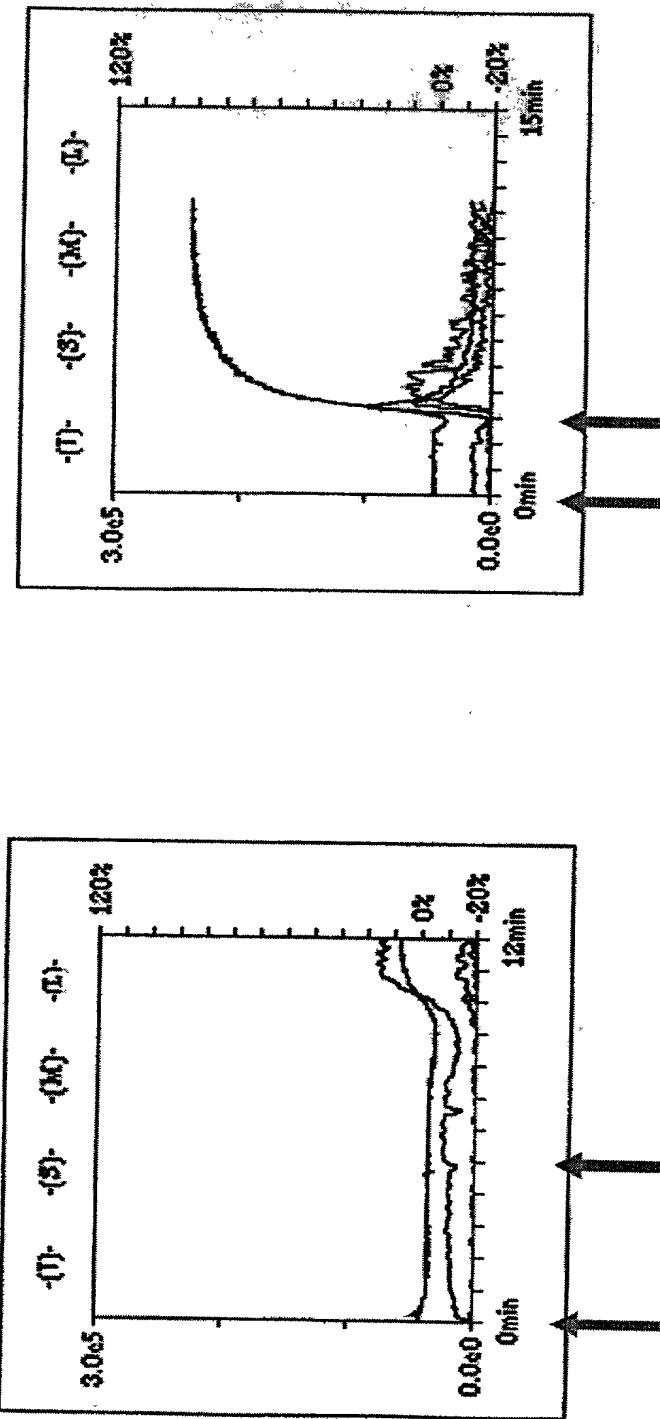


FIGURE 22

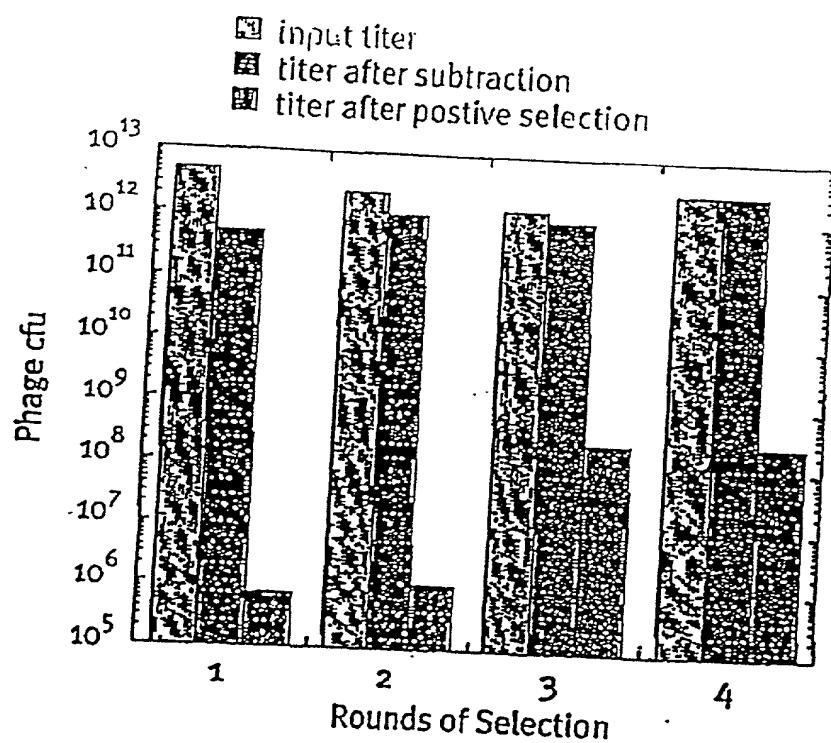


FIGURE 23

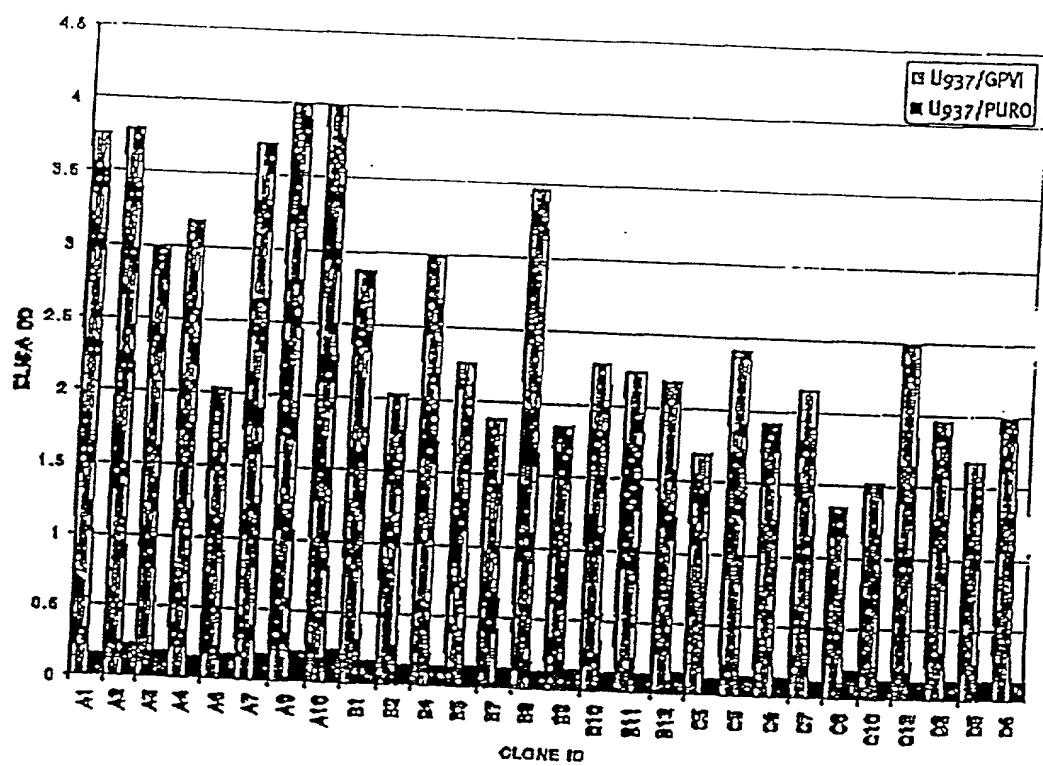
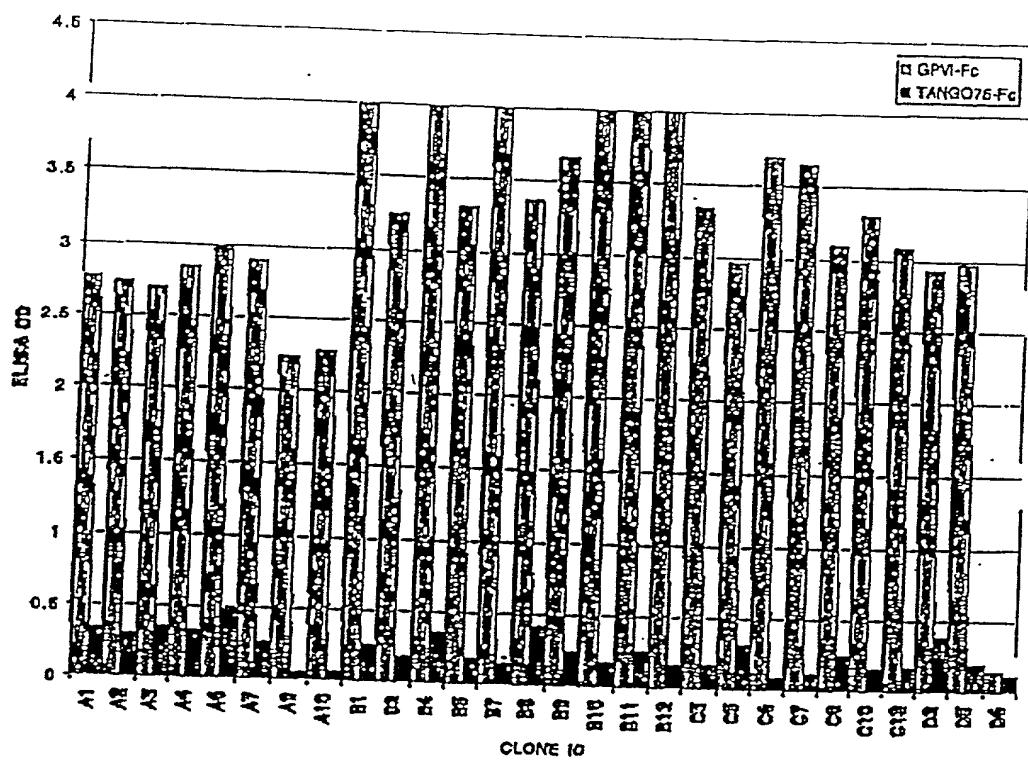


FIGURE 24a



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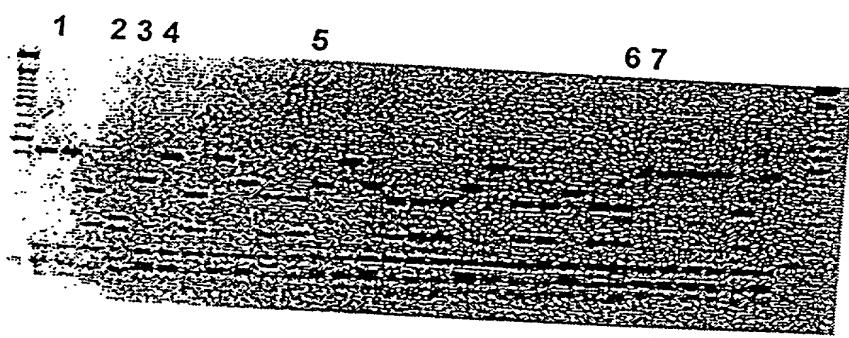
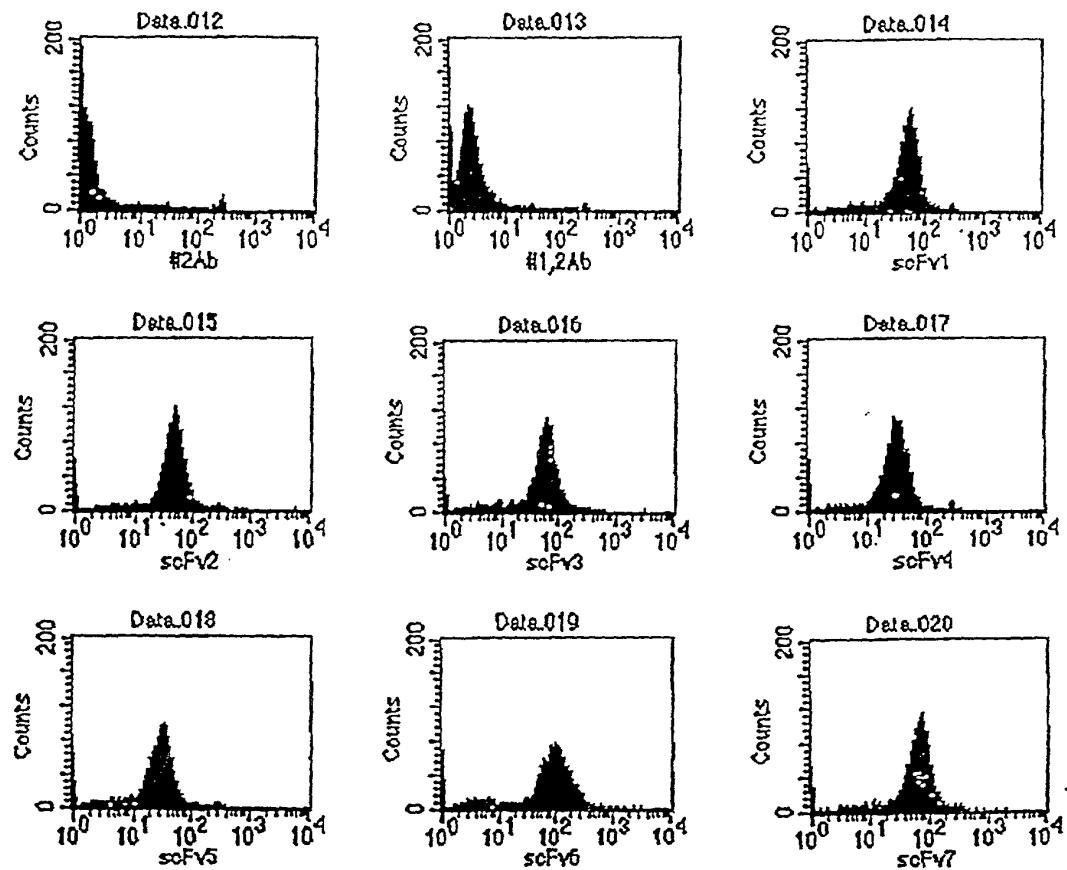


FIGURE 25

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scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C3
scFv5:C9
scFv6:C10
scFv7:A10

FIGURE 26

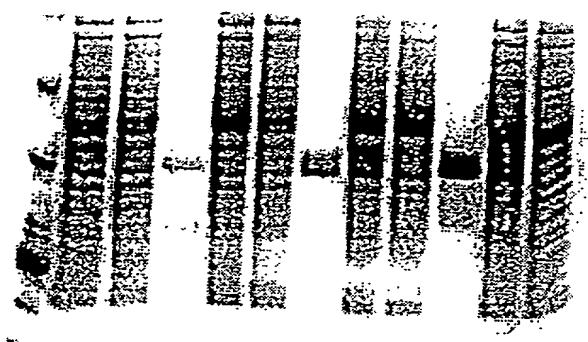
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A4

A9

A10



B4

C3

C9

C10

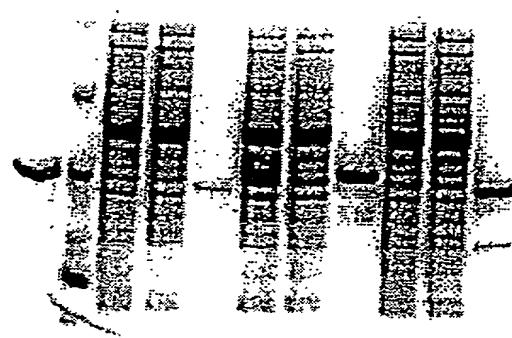


FIGURE 27

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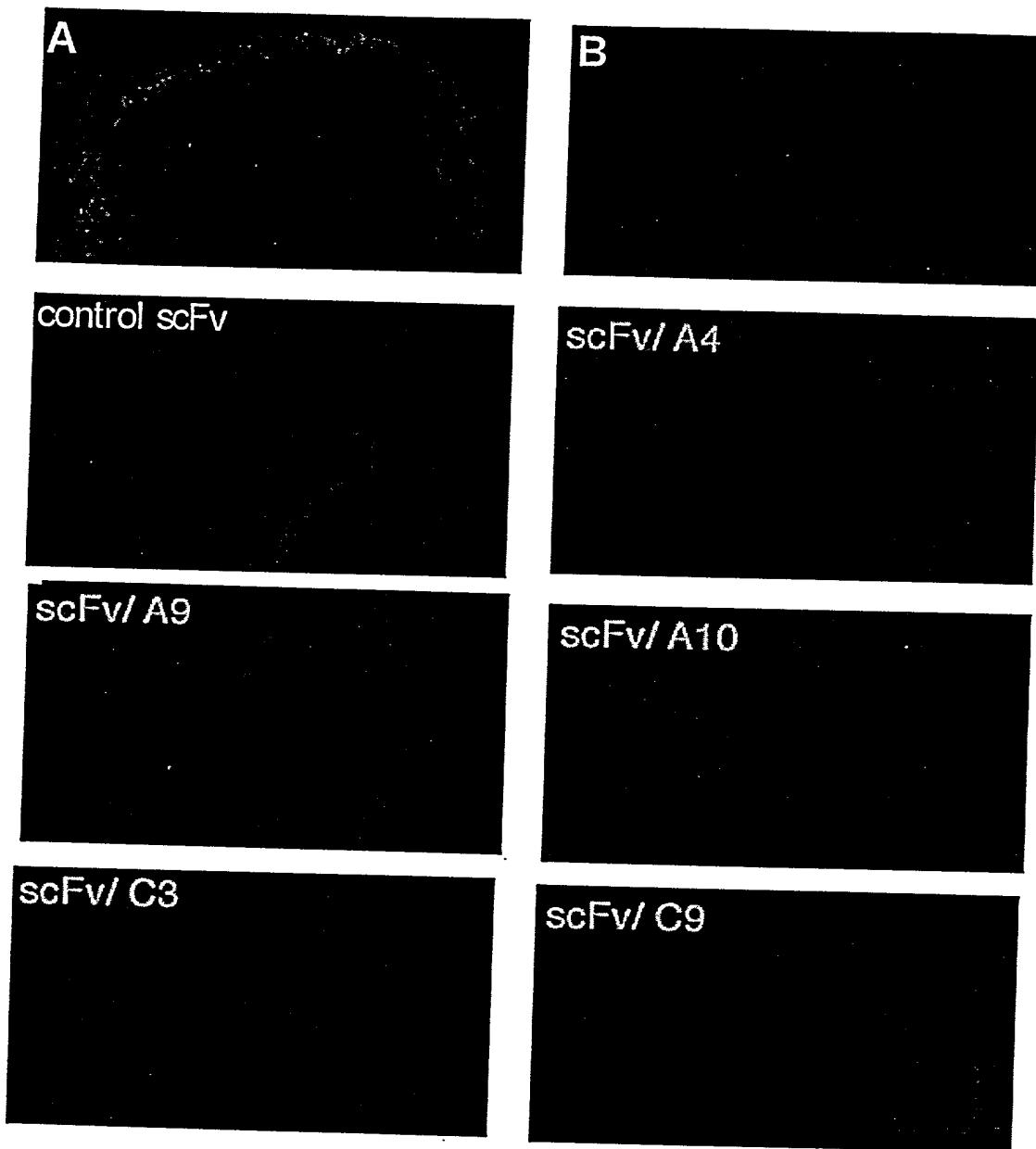


FIGURE 28

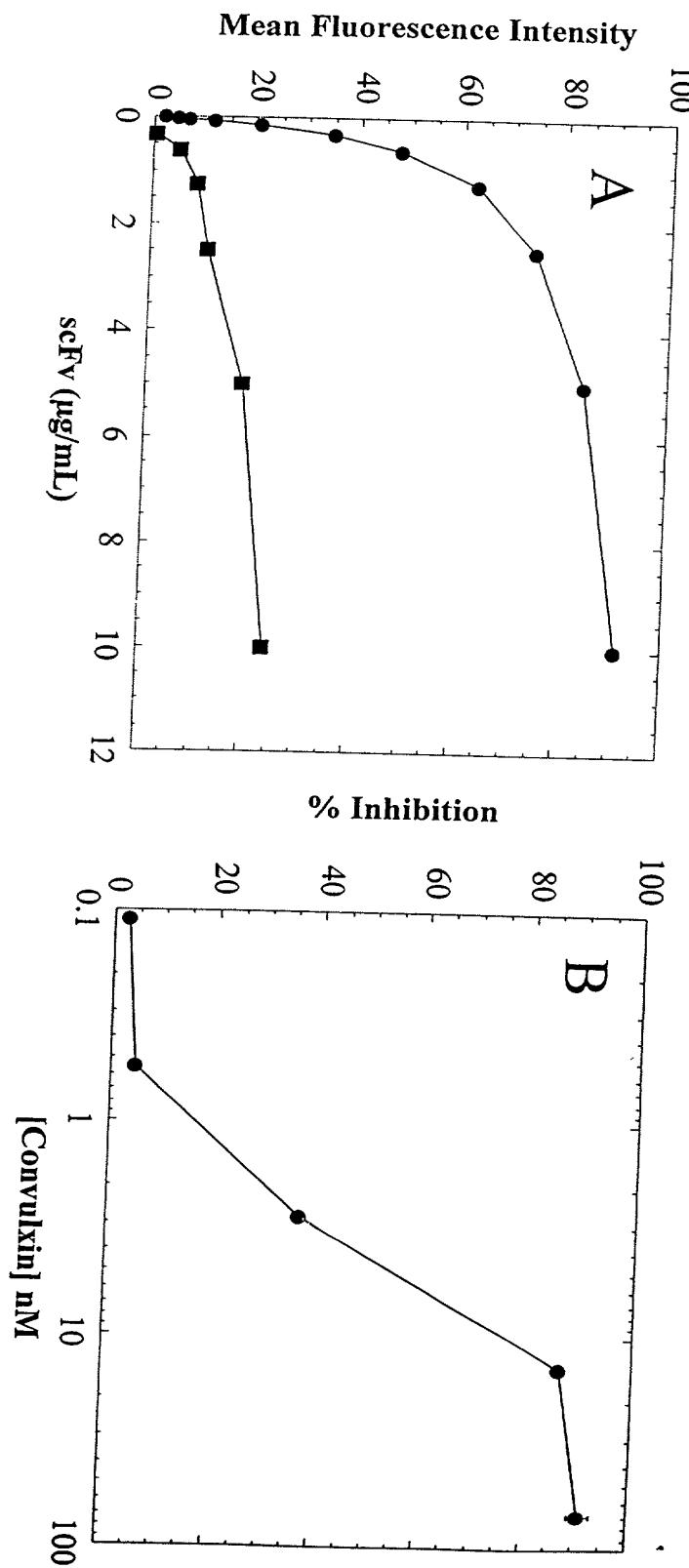


FIGURE 29

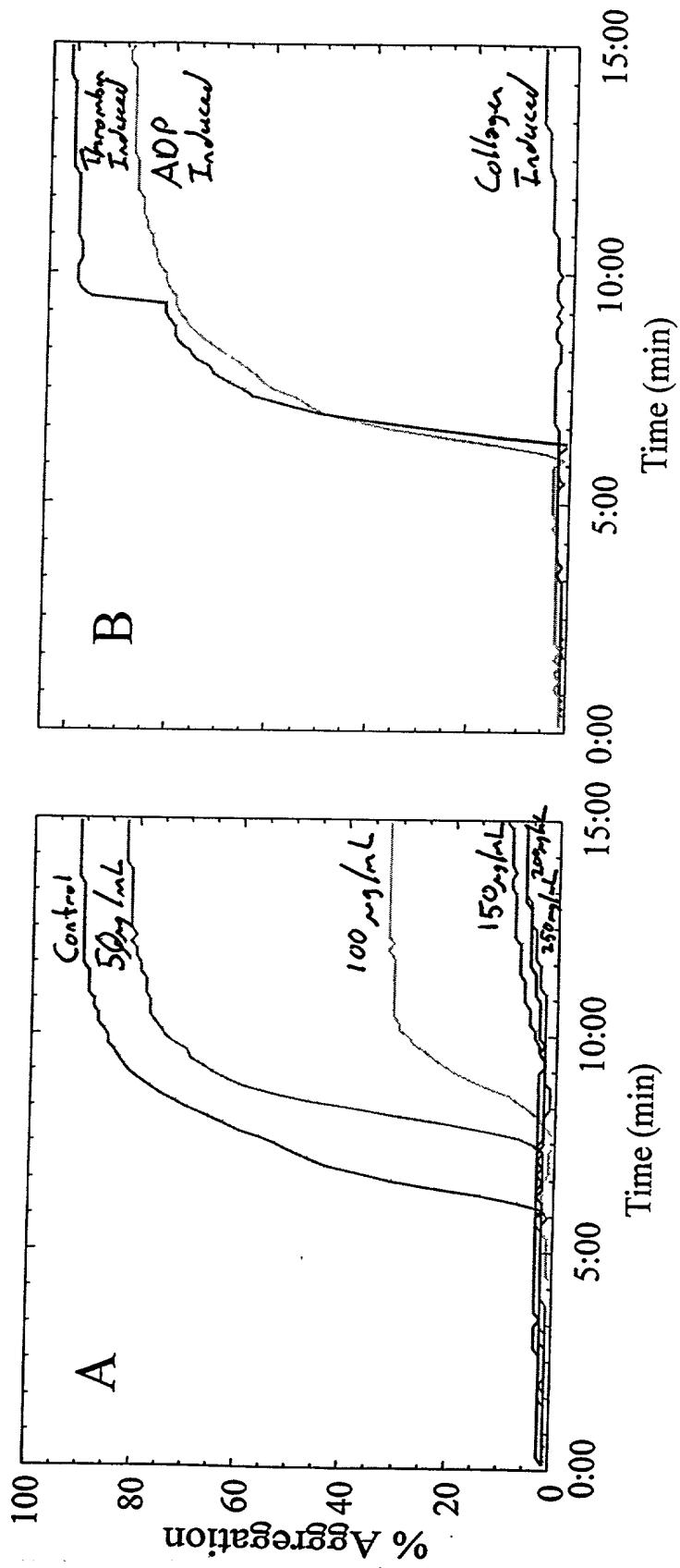


FIGURE 30